

Please replace the paragraph starting with “This application claims priority...” at page 1, line 5, with the following amended paragraph:

Please amend Table 2 on page 9 as follows:

Comparison between a NOV1 polypeptide and thymosin beta-10 from human

Please amend Table 3 on page 9 as follows:

Multiple Sequence alignment of a NOV1 polypeptide and the thymosin beta family

(Black outlined amino acids indicate potential regions of conserved sequence; grayed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs. Sequences may be referenced by the SWISSPROT or TREMBL ID.)

	10	20	30	40	
thymosin beta family motif
NOV1 (2-38)	ADKPD	IGETASFN	KKLTETQ	EN	(SEQ ID NO:35)
TYB0_HUMAN(1-38)	ADKPD	IGETASFD	KKLTETQ	ENIL	(SEQ ID NO:2)
TYB9_BOVIN(1-40)	ADKPD	IGETASFD	KKLTETQ	ENIL	(SEQ ID NO:36)
TYB9_PIG(1-40)	ADKPD	IGETASFD	KKLTETQ	ENIL	(SEQ ID NO:37)
TYB4_HUMAN(1-40)	ADKPD	IGETASFD	KKLTETQ	ENIL	(SEQ ID NO:38)
TYB4_MOUSE(7-47)	SDKPD	MAEIEKFD	SKLKKTT	ETQ	(SEQ ID NO:39)
TYB4_RABIT(1-40)	SDKPD	MAEIEKFD	SKLKKTT	ETQ	(SEQ ID NO:40)
TYB4_XENLA(1-39)	SDKPD	MAEIEKFD	SKLKKTT	ETQ	(SEQ ID NO:41)
TYBY_HUMAN(1-40)	SDKPD	MAEIEKFD	SKLKKTT	ETQ	(SEQ ID NO:42)
TYBA_ONCMY(1-40)	SDKPD	MAEIEKFD	SKLKKTT	ETQ	(SEQ ID NO:43)
TYBB_ONCMY(1-40)	SDKEN	LEEVASF	DKSKLKK	TTETQ	(SEQ ID NO:44)
TYBB_LATJA(1-40)	SDKPD	LAEEVSN	FDKSKLKK	TTETQ	(SEQ ID NO:45)
P97563_RAT(1-39)	SDKPD	LAEEVSN	FDKSKLKK	TTETQ	(SEQ ID NO:46)
TYBN_HUMAN(1-38)	MSDKP	DLSEVET	FDKSKLKK	TTETQ	(SEQ ID NO:47)
O97428_DROME(95-129)	SDKPD	LSVEKFD	RSKLKKTT	ETQ	(SEQ ID NO:48)
O97428_DROME(59-89)	LAGI	ENFD	AKKLKHT	ETNEKN	(SEQ ID NO:49)
	GLTAF	NQNLKHT	ETNEKN	NPLD	(SEQ ID NO:50)

Table 4.
PFAM alignment of a NOV1 polypeptide to the consensus sequence of the thymosin beta family

Please amend Table 6 beginning on page 13 as follows:

NOV2:	1	MAPARGRLPPALWVVTAATAAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSEINEV	60
Sbjct:	1	MAPARARLSPALWVVTAATAA-TCVSAGRGEVNLLDTSTIHGDWGWLTYPAHGWDSEINEV	59
NOV2:	61	DESFPQPIHTYQVCNVMSPNQNNLRTSWVPRDGARRVYAIEKFTLRDCNSMPGVLGTCKE	120
Sbjct:	60	DESFRIPIHTYQVCNVMSPNQNNLRTNWVPRDGARRVYAIEKFTLRDCNSIPGVLGTCKE	119
NOV2:	121	TFNLYYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTFVRSVGPLSKRG	180
Sbjct:	120	TFNLHYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTFVRGVGPGLSKRG	179
NOV2:	181	FYLAFQDIGACLAAILSLRIYYKKCPAMVRNLAASFVAVTGADSSSLVEVRGQCVRHSEER	240
Sbjct:	180	FYLAFQDIGACLAAILSLRIYYKKCPAMVRNLAASFVAVTGADSSSLVEVRGQCVRHSEER	239
NOV2:	241	DTPKMYCSAEGEWLVPIGKCVCASAGYEERRDACVACELGFYSAPGDQLCARCPPHSLSA	300
Sbjct:	240	DTPKMYCSAEGEWLVPIGKCVCASAGYEERRDACLACELGFYSAPGDQLCARCPPHSLSA	299
NOV2:	301	APAAQACHCDLSYYRAALDPSSACTRPSPAPVNLISSVNGTSVTLEWAPPLDPGGRSDI	360
Sbjct:	300	TPAAQTCRCDSL YYRAALDPSSAACTRPSPAPVNLISSVNGTSVTLEWAPPLDPGGRSDI	359
NOV2:	361	TYNVAVCRRCPWALSACEACSGTRFVPQQTSLVQASLLVANLLAHMNYSFWEAVNGVSD	420


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      TFNLVYLESDRDLGASTQESQFLKIDTIAADESFTCADLGVRRLKLNTEVRSVGPPLSKRG
Sbjct: 121 TFNLVYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPPLSKRG 180

NOV2 : 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAASFSEAVTGADSSSLVEVRGQCVRHSEER 240
      |||
Sbjct: 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAASFSEAVTGADSSSLVEVRGQCVRHSEER 240

NOV2 : 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300
      |||
Sbjct: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300

NOV2 : 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360
      |||
      APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI
Sbjct: 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360

NOV2 : 361 TYNACRRCPWALSRCACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
      |||
Sbjct: 361 TYNACRRCPWALSRCACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420

NOV2 : 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480
      |||
Sbjct: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480

NOV2 : 481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
      |||
      DKEMQSYSTLKAVTTRATVSGLKPGTRYVVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT
Sbjct: 481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540

NOV2 : 541 RTIVWICLTITGLVVLVLLLLICKKRHCYSGKAFQDSDEEKMHYQNGQAPPVFLPLHHP 600
      |||
Sbjct: 541 RTIVWICLTITGLVVLVLLLLICKKRHCYSGKAFQDSDEEKMHYQNGQAPPVFLPLHHP 600

NOV2 : 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRRLRVPQR 660
      |||
Sbjct: 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRRLRVPQR 660

NOV2 : 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIIRLEGVVTGRRLAMIVTEYMENG 720
      |||
Sbjct: 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIIRLEGVVTGRRLAMIVTEYMENG 720

NOV2 : 721 LDTFLRTHDGQFTIMQLVGMLRGVAGMRYLSDLGYPVHRDLAARNVLVDSNLVCKVSDFG 780
      |||
Sbjct: 721 LDTFLRTHDGQFTIMQLVGMLRGVAGMRYLSDLGYPVHRDLAARNVLVDSNLVCKVSDFG 780

NOV2 : 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
      |||
Sbjct: 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840

NOV2 : 841 NMTNRDVISSVEEGYRLPAPMGC PHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
      |||
Sbjct: 841 NMTNRDVISSVEEGYRLPAPMGC PHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900

NOV2 : 901 SLRATATVSRCPPPAFVRSCFDLRGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960
      |||
Sbjct: 901 SLRATATVSRCPPPAFVRSCFDLRGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960

NOV2 : 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
      |||
Sbjct: 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:53)

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Please amend the paragraph beginning at line 4 in Table 7 on page 16 as follows:

Table 7 shows multiple sequence alignment of the NOV2 ephrim type-A receptor 8-like protein of the invention, shown as AL035703 Spliced2 , with similar proteins. The

various aligned proteins are as follows: AL035703 Spliced2 (SEQ ID NO:5) with several proteins: EPA8 Mouse (SEQ ID NO:54), EPA5 Human (SEQ ID NO:55) and EPA5 Chick (SEQ ID NO:56). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Please amend the paragraph beginning at line 5 in Table 9 on page 20 as follows:

Table 9 shows sequence alignment between a NOV3 polypeptide with several members of the human fibronectin leucine repeat transmembrane family: AAF28461.1|AF169 (SEQ ID NO:57), AAF28460.1|AF169 (SEQ ID NO:58) and AAF28459.1|AF169 (SEQ ID NO:59). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Please amend Table 9. continued on page 21 as follows:

TABLE 9. continued TABLE 9A.

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>ref|NP_037412.1| fibronectin leucine rich transmembrane protein 1
gb|AAF28459.1|AF169675_1 (AF169675) leucine-rich repeat transmembrane protein
FLRT1 [Homo sapiens]
Length = 674
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Score = 1365 bits (3494), Expect = 0.0
Identities = 673/674 (99%), Positives = 674/674 (99%)
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NOV3: 1  MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60
      |||
Sbjct: 1  MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60

NOV3: 61  DNGFIYCNDRLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120
      |||
Sbjct: 61  DNGFIYCNDRLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120

NOV3: 121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNSVSTVSIEEDAFADSKQLK 180
      |||
Sbjct: 121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNSVSTVSIEEDAFADSKQLK 180

NOV3: 181  LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240
      |||
Sbjct: 181  LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240

NOV3: 241  DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300
      |||
Sbjct: 241  DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300

NOV3: 301  LSNNNLTTLP RGLFDDLG NLAQLLRNNPWF CGCNLMWLRD WVKARAAVNVNVRGLMCQGP 360
      |||
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Sbjct: 301 LSNNNLTTLPRGLFDDLG NLAQ LLLRNNPWFCGCNLMWLRD WVKARAAVVNV RGLMCQGP 360
NOV3: 361 EKVRGMAIKDITSEMDEC FETGPQGGVANAAAKTTASNHASATTPQGS LFTLKAKRPGLR 420
      |||||||||||||||||||
Sbjct: 361 EKVRGMAIKDITSEMDEC FETGPQGGVANAAAKTTASNHASATTPQGS LFTLKAKRPGLR 420
NOV3: 421 LPDSNIDYPMATGDGAKTLAIHV KALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI 480
      |||||||||||||||||||
Sbjct: 421 LPDSNIDYPMATGDGAKTLAIHV KALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI 480
NOV3: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETS NAYVADETPVCAKAETADSYGPTTTLN 540
      |||||||||||||||||||
Sbjct: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETS NAYVADETPVCAKAETADSYGPTTTLN 540
NOV3: 541 QEQNAGPMASLPLAGIIGGAVALVFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDY 600
      |||||||||||||||||||
Sbjct: 541 QEQNAGPMASLPLAGIIGGAVALVFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDY 600
NOV3: 601 MESGTTKDN SILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCKATH TIGYGTTRG 660
      |||||||||||||||||||
Sbjct: 601 MESGTTKDN SILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCKATH TIGYGTTRG 660
NOV3: 661 YRDGGIPDIDYSY T 674 (SEQ ID NO:7)
      |||||||||||
Sbjct: 661 YRDGGIPDIDYSY T 674 (SEQ ID NO:60)

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Please amend the paragraph beginning at line 6 in Table 10 on page 22 as follows:

Table 10 shows sequence alignment between a NOV3 polypeptide with various fibromodulins: ACC NO: O43408 (SEQ ID NO:61), ACC NO: AP000597 (SEQ ID NO:7), ACC NO: O43155 (SEQ ID NO:62), ACC NO: O42235 (SEQ ID NO:63) and FMOD Bovin FM (SEQ ID NO:64). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Please insert sequence listing pages 1-47 at the end of the specification.